**Amendments to the Specification:**

Please replace the paragraph beginning at page 4, line 10 with the following amended paragraph:

Figures 2A-2B show the genetic organization of the *cst-I* locus from OH4384 and comparison of the LOS biosynthesis loci from OH4384 and NCTC 11168. The distance between the scale marks is 1 kb. Figure 2A shows a schematic representation of the OH4384 *cst-I* locus, based on the nucleotide sequence which is available from GenBank (#AF130466). The partial *prfB* gene is somewhat similar to a peptide chain release factor (GenBank #AE000537) from *Helicobacter pylori*, while the *cysD* gene and the partial *cysN* gene are similar to *E. coli* genes encoding sulfate adenylyltransferase subunits (GenBank #AE000358). Figure 2B shows a schematic representation of the OH4384 LOS biosynthesis locus, which is based on the nucleotide sequence from GenBank (#AF130984). The nucleotide sequence of the OH4382 LOS biosynthesis locus is identical to that of OH4384 except for the *cgtA* gene, which is missing an "A" (see text and GenBank #AF167345). The sequence of the NCTC 11168 LOS biosynthesis locus is available from the Sanger Centre ~~(URL:http//www.sanger.ac.uk/Projects/C_jejuni/)~~ (www.sanger.ac.uk/Projects/C_jejuni/). Corresponding homologous genes have the same number with a trailing "a" for the OH4384 genes and a trailing "b" for the NCTC 11168 genes. A gene unique to the OH4384 strain is shown in black and genes unique to NCTC 11168 are shown in grey. The OH4384 ORF's #5a and #10a are found as an in-frame fusion ORF (#5b/10b) in NCTC 11168 and are denoted with an asterisk (*). Proposed functions for each ORF are found in Table 4.

Please replace the paragraph bridging pages 4 and 5 with the following amended paragraph:

Figure 3 shows an alignment of the deduced amino acid sequences for the sialyltransferases. The OH4384 *cst-I* gene (SEQ ID NO:48, first 300 residues), OH4384 *cst-II* gene (SEQ ID NO:3, identical to OH4382 *cst-II*), O:19 (serostrain) *cst-II* gene (SEQ ID NO:9, GenBank #AF167344) , NCTC 11168 *cst-II* gene (SEQ ID NO: 10) and an *H. influenzae* putative ORF (SEQ ID

NO:49, GenBank #U32720) were aligned using the ClustalX alignment program (Thompson *et al.* (1997) *Nucleic Acids Res.* **25,** 4876-82). The shading was produced by the program GeneDoc (Nicholas, K. B., and Nicholas, H. B. (1997) ~~URL: http://www.cris.com/~ketchup/genedoc.shtml~~ www.cris.com/~ketchup/genedoc.shtml).

Please replace the paragraph beginning at page15, line 11 with the following amended paragraph:

Examples of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.* (1990) *J. Mol. Biol.* 215: 403-410 and Altschuel *et al.* (1977) *Nucleic Acids Res.* 25: 3389-3402, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information ~~(http://www.ncbi.nlm.nih.gov/)~~ (www.ncbi.nlm.nih.gov/). For example, the comparisons can be performed using a BLASTN Version 2.0 algorithm with a wordlength (W) of 11, G=5, E=2, q= -2, and r = 1., and a comparison of both strands. For amino acid sequences, the BLASTP Version 2.0 algorithm can be used, with the default values of wordlength (W) of 3, G=11, E=1, and a BLOSUM62 substitution matrix. (*see* Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)).

Please replace the paragraph beginning at page 49, line 2 with the following amended paragraph:

The primers used to amplify the LPS biosynthesis locus of *C. jejuni* OH4384 were based on preliminary sequences available from the website ~~(URL: http://www.sanger.ac.uk/Projects/C_jejuni/)~~ ~~(www.sanger.ac.uk/Projects/C_jejuni/)~~ of the *C. jejuni* sequencing group (Sanger Centre, UK) who sequenced the complete genome of the strain NCTC11168. The primers CJ-42 and CJ-43 (all primers sequences are described in Table 2) were used to amplify an 11.47 kb locus using the Expand™ long template PCR system. The PCR product was purified on a S-300 spin column (Pharmacia Biotech) and completely sequence on

both strands using a combination of primer walking and sub-cloning of *Hind*III fragments. Specific ORF's were amplified using the primers described in Table 2 and the Pwo DNA polymerase. The PCR products were digested using the appropriate restriction enzymes (*see* Table 2) and were cloned in pCWori+.

Please replace the paragraph beginning at page 53, line 15 with the following amended paragraph:

Analysis of the preliminary sequence data available at the website of the *C. jejuni* NCTC 11168 sequencing group (Sanger Centre, UK ~~(http://www.sanger.ac.uk/ Projects /C_jejuni/)~~ (www.sanger.ac.uk/ Projects /C_jejuni/)) revealed that the two heptosyltransferases involved in the synthesis of the inner core of the LPS were readily identifiable by sequence homology with other bacterial heptosyltransferases. The region between the two heptosyltransferases spans 13.49 kb in NCTC 11168 and includes at least seven potential glycosyltransferases based on BLAST searches in GenBank. Since no structure is available for the LOS outer core of NCTC 11168, it was impossible to suggest functions for the putative glycosyltransferase genes in that strain.

Please replace the paragraph beginning at page 56, line 1 with the following amended paragraph:

The sequence of the *C. jejuni* NCTC 11168 ORFs can be obtained from the Sanger Centre ~~(URL:http//www.sanger.ac.uk/Projects/C_jejuni/ )~~ (www.sanger.ac.uk/Projects/C_jejuni/ ).